

CLAIMS

We claim:

1. A method for generating a secondary library of scaffold protein sequences comprising:
 - a) generating a probability distribution table of amino acid residues in a plurality of
5 variant positions from a force field calculation; and
 - b) combining a plurality of said amino acid residues to generate a secondary library of secondary sequences; wherein at least one of said secondary sequences is different from said primary sequences.
- 10 2. A method according to claim 1 further comprising synthesizing a plurality of said secondary sequences.
3. A method according to claim 2 wherein said synthesizing is done by multiple PCR with pooled oligonucleotides.
4. A method according to 3 wherein said pooled oligonucleotides are added in equimolar amounts.
- 15 5. A method according to claim 3 wherein said pooled oligonucleotides are added in amounts that correspond to the frequency of the mutation.
6. A method according to claim 3 wherein said pooled oligonucleotides are pooled in relative amounts.

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